

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Johnson, Howard M.  
Pontzer, Carol H.

(ii) TITLE OF INVENTION: Interferon Tau Compositions and  
Methods of Use

(iii) NUMBER OF SEQUENCES: 44

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94306

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Filed herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/455,021  
(B) FILING DATE: 31-MAY-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/438,753  
(B) FILING DATE: 10-MAY-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/139,891  
(B) FILING DATE: 19-OCT-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/847,741
- (B) FILING DATE: 09-MAR-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/318,050
- (B) FILING DATE: 02-MAR-1989

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/969,890
- (B) FILING DATE: 30-OCT-1992

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dehlinger, Peter J.
- (B) REGISTRATION NUMBER: 28,006
- (C) REFERENCE/DOCKET NUMBER: 5600-0001.36

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-324-0880
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ovis aries
- (B) STRAIN: Domestic
- (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
- (F) TISSUE TYPE: Trophectoderm

(G) CELL TYPE: Mononuclear trophectoderm cells

(vii) IMMEDIATE SOURCE:

(B) CLONE: oTP-1a

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..516

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Ott, Troy L

Van Heeke, Gino

Johnson, Howard M

Bazer, Fuller W

(B) TITLE: Cloning and Expression in Saccharomyces cerevisiae of a Synthetic Gene for the Type I Trophoblast Interferon Ovine Trophoblast Protein-1: Purification and Antiviral Activity

(C) JOURNAL: J. Interferon Res.

(D) VOLUME: 11

(F) PAGES: 357-364

(G) DATE: 1991

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA 48  
Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys  
1 5 10 15

CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC 96  
Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp  
20 25 30

CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG 144  
Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu  
35 40 45



(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of a mature  
OvIFNtau protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys  
1 5 10 15

Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp  
20 25 30

Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu  
35 40 45

Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser  
50 55 60

Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr  
65 70 75 80

Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu  
85 90 95

Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly  
100 105 110

Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr  
115 120 125

Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val  
130 135 140

Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys  
145 150 155 160

Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding  
a mature human interferon-tau protein, HuIFN $\tau$ aul.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|  |     |
|--|-----|
| TGTGACTTGT CTCAAACCA CGTTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA   | 60  |
| ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTTGCCTCAG  | 120 |
| GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG  | 180 |
| TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCACC  | 240 |
| TTGTTGGAAC AGCTCAGAAC CGGTTTGCAC CAACAATTGG ACAACTTGGA TGCATGTTTG  | 300 |
| GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG  | 360 |
| AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGA CTGTGCT | 420 |
| TGGGAAACCG TCGTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA   | 480 |
| AGATTACGTA TGATGGACGG TGACTTGTCG AGCCCA                            | 516 |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence for a mature  
HuIFNtau protein, HuIFNtau1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg  
1 5 10 15

Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp  
20 25 30

Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu  
35 40 45

Gln, Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser  
50 55 60

Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr  
65 70 75 80

Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu  
85 90 95

Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly  
100 105 110

Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His  
115 120 125

Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val  
130 135 140

Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu  
145 150 155 160

Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 1-37  
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys  
5 10 15  
Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp  
20 25 30  
Arg Lys Asp Phe Gly  
35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 34-64  
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln  
5 10 15



Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 62-92  
 of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp  
 5 10 15

Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 90-122  
 of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Gln Gln Leu Asp His Leu Asp Thr Cys Arg Gly Gln Val Met Gly  
5 10 15

Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile Val Thr Val Lys  
20 25 30

Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 119-150  
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Tyr Leu Gln Glu Lys  
5 10 15

Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg  
20 25 30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 139-172  
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val  
5 10 15

Ser Thr Thr Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn  
20 25 30

Ser Pro

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau1 Human Interferon Tau coding  
sequence with a leader sequence.

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC TAC  
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
1 5 10 15

48

GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC GTG CTG 96  
 Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu  
 20 25 30

GTT GGC AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC 144  
 Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
 35 40 45

CCT CGC TTT TGT CTG CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA 192  
 Pro Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu  
 50 55 60

ATG GTG GAG GGC GGC CAG CTC CAG GAG GCC CAG GCC ATC TCT GTG CTC 240  
 Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
 65 70 75 80

CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA GAG CAC TCC 288  
 His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
 85 90 95

TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT GGA CTC 336  
 Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu  
 100 105 110

CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA 384  
 His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
 115 120 125

GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG 432  
 Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
 130 135 140

AGG TAC TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC 480  
 Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
 145 150 155 160

GAC TGC GCC TGG GAA ACC GTC AGA CTG GAA ATC ATG AGA TCC TTC TCT 528  
 Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser  
 165 170 175

TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA ATG ATG GAT GGA GAC CTG 576  
 Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu  
 180 185 190

AGC TCA CCT TGA 588  
 Ser Ser Pro  
 195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
 of SEQ ID NO:11 (HuIFNtau1).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
 1 5 10 15  
 Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu  
 20 25 30  
 Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
 35 40 45  
 Pro Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu  
 50 55 60  
 Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
 65 70 75 80  
 His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
 85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu  
 100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
 115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
 130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
 145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser  
 165 170 175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu  
 180 185 190

Ser Ser Pro  
 195

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: 25-mer synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTGTCTGCA GGACAGAAAA GACTT

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: 25-mer synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTGAATTCT GACGATTTC CAGGC

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
1-37 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Asp | Leu | Ser | Gln | Asn | His | Val | Leu | Val | Gly | Arg | Lys | Asn | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Asp | Glu | Met | Arg | Arg | Leu | Ser | Pro | Arg | Phe | Cys | Leu | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Arg | Lys | Asp | Phe | Ala |
|     |     |     |     | 35  |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
34-64 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Phe | Ala | Leu | Pro | Gln | Glu | Met | Val | Glu | Gly | Gly | Gln | Leu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Ala | Gln | Ala | Ile | Ser | Val | Leu | His | Glu | Met | Leu | Gln | Gln | Ser |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
62-92 of SEQ ID NO:4



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp  
1 5 10 15

Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln  
20 25 30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
90-122 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
1 5 10 15

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp  
1 5 10 15

Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln  
20 25 30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
90-122 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
1 5 10 15

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

**Q**uestions **A**nswers **C**onclusions **E**xercises **P**roblems **S**olutions **T**ables **V**ocabulary **I**ndex

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg  
20 25 30

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu Ser  
20 25 30

125

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|   |     |
|---|-----|
| C CAG GAG ATG GTG GAG GGC GGC CAG CTC CAG GAG GCC CAG GCC ATC   | 46  |
| Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile     |     |
| 1 5 10 15   |     |
| TCT GTG CTC CAC AAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA | 94  |
| Ser Val Leu His Lys Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr |     |
| 20 25 30  |     |
| GAG CGC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC | 142 |
| Glu Arg Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg |     |
| 35 40 45  |     |
| ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG GAC GCC TGC CTG GGG CAG | 190 |
| Thr Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln |     |
| 50 55 60  |     |
| GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG | 238 |
| Val Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu |     |
| 65 70 75  |     |

GCC GTG AAG AGC TAC TTC CAG GGC ATC CAT ATC TAC CTG CAA GAG AAG  
 Ala Val Lys Ser Tyr Phe Gln Gly Ile His Ile Tyr Leu Gln Glu Lys  
 80 85 90 95

286

GGA TAC AGC GAC T  
 Gly Tyr Ser Asp

299

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
 of SEQ ID NO:21 (HuIFNtau6).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser  
 1 5 10 15  
 Val Leu His Lys Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu  
 20 25 30  
 Arg Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr  
 35 40 45  
 Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val  
 50 55 60  
 Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala  
 65 70 75 80  
 Val Lys Ser Tyr Phe Gln Gly Ile His Ile Tyr Leu Gln Glu Lys Gly  
 85 90 95  
 Tyr Ser Asp

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau7

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| C   | CAG | GAG | ATG | GTG | GAG | GTC | AGC | CAG | TTC | CAG | GAG | GCC | CAG | GCC | ATT | 46  |
|     | Gln | Glu | Met | Val | Glu | Val | Ser | Gln | Phe | Gln | Glu | Ala | Gln | Ala | Ile |     |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TCT | GTG | CTC | CAT | GAG | ATG | CTC | CAG | CAG | AGC | TTC | AAC | CTC | TTC | CAC | AAA | 94  |
| Ser | Val | Leu | His | Glu | Met | Leu | Gln | Gln | Ser | Phe | Asn | Leu | Phe | His | Lys |     |
|     |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAG | CGC | TCC | TCT | GCT | GCC | TGG | GAC | ACT | ACC | CTC | CTG | GAG | CAG | CTC | CTC | 142 |
| Glu | Arg | Ser | Ser | Ala | Ala | Trp | Asp | Thr | Thr | Leu | Leu | Glu | Gln | Leu | Leu |     |
|     |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACT | GGA | CTC | CAT | CAG | CAG | CTG | GAT | GAC | CTG | GAT | GCC | TGT | CTG | GGG | CAG | 190 |
| Thr | Gly | Leu | His | Gln | Gln | Leu | Asp | Asp | Leu | Asp | Ala | Cys | Leu | Gly | Gln |     |
|     |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |

TTG ACT GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238  
 Leu Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu  
 65 70 75

GCC GTG AAG AGC TAC TTC CAG GGC ATC CAT GTC TAC CTG CAA GAG AAG 286  
 Ala Val Lys Ser Tyr Phe Gln Gly Ile His Val Tyr Leu Gln Glu Lys  
 80 85 90 95

GG 288

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
 of SEQ ID NO:23 (HuIFNtau7).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln Glu Met Val Glu Val Ser Gln Phe Gln Glu Ala Gln Ala Ile Ser  
 1 5 10 15  
 Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Lys Glu  
 20 25 30  
 Arg Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Leu Thr  
 35 40 45  
 Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Leu  
 50 55 60  
 Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala  
 65 70 75 80

Val Lys Ser Tyr Phe Gln Gly Ile His Val Tyr Leu Gln Glu Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau4

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|   |   |    |
|---|---|----|
| C   | CAG GAG ATG GTG GAG GGT GGC CAG CTC CAG GAG GCC CAG GCC ATC | 46 |
|   | Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile |    |
| 1   | 5 10 15   |    |
| TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA | 94  |    |
| Ser Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr |   |    |
| 20 25 30  |   |    |
| GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC | 142   |    |
| Glu His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg |   |    |
| 35 40 45  |   |    |



ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG 190  
Thr Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln  
50 55 60

GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238  
Val Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu  
65 70 75

GCC ATG AAG ACG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG  
Ala Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys 286  
80 85 90 95

GGA TAT AGT GAC TGC GCC TGG  
Gly Tyr Ser Asp Cys Ala Trp  
100

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
of SEQ ID NO:25 (HuIFNtau4).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser  
1 5 10 15

Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu  
20 25 30

His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr  
35 40 45

Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val  
 50 55 60  
 Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala  
 65 70 75 80  
 Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly  
 85 90 95  
 Tyr Ser Asp Cys Ala Trp  
 100

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau5

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

C CAG GAG ATG GTG GAG GGT GGC CAG CTC CAG GAG GCC CAG GCC ATC  
 Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile  
 1 5 10 15

46

TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA 94  
 Ser Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr  
                     20                    25                    30

GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC 142  
 Glu His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg  
                     35                    40                    45

ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG 190  
 Thr Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln  
                     50                    55                    60

GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238  
 Val Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu  
                     65                    70                    75

GCC ATG AAG ACG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG 286  
 Ala Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys  
                     80                    85                    90                    95

GGA TAT AG 294  
 Gly Tyr

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
 of SEQ ID NO:27 (HuIFNtau5).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser  
     1                    5                    10                    15





(A) NAME/KEY: Modified-site

(B) LOCATION: 115-117

(D) OTHER INFORMATION: /note= "to allow expression of the  
encoded protein this site can be modified  
to encode an amino acid, e.g., Gln"

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
of SEQ ID NO:29 (HuIFNtau2).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg Leu  
1 5 10 15  
Leu Asp Gln Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp Arg  
20 25 30  
Lys Asp Phe Ala Leu Pro Xaa Glu Met Val Glu Gly Gly Gln Leu Gln  
35 40 45  
Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser Phe  
50 55 60  
Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr Leu  
65 70 75 80  
Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu Asp  
85 90 95  
Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly Arg  
100 105 110

Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His Val  
115 120 125

(A) NAME/KEY: Modified-site

(B) LOCATION: 39

(D) OTHER INFORMATION: /note= "where Xaa a selected amino acid,  
for example, Gln"

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|   |     |
|---|-----|
| ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC TAC | 48  |
| Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr |     |
| 1 5 10 15   |     |
| GGC CCG GGA GGA TCC CTG CGG TGT GAC CTG TCT CAG AAC CAC GTG CTG | 96  |
| Gly Pro Gly Gly Ser Leu Arg Cys Asp Leu Ser Gln Asn His Val Leu |     |
| 20 25 30  |     |
| GTT GGC AGC CAG AAC CTC AGG CTC CTG GGC CAA ATG AGG AGA CTC TCC | 144 |
| Val Gly Ser Gln Asn Leu Arg Leu Leu Gly Gln Met Arg Arg Leu Ser |     |
| 35 40 45  |     |
| CTT CGC TTC TGT CTG CAG GAC AGA AAA GAC TTC GCT TTC CCC CAG GAG | 192 |
| Leu Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Phe Pro Gln Glu |     |
| 50 55 60  |     |
| ATG GTG GAG GGT GGC CAG CTC CAG GAG GCC CAG GCC ATC TCT GTG CTC | 240 |
| Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu |     |
| 65 70 75 80   |     |
| CAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA GAG CAC TCC | 288 |
| His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser |     |
| 85 90 95  |     |
| TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT GGA CTC | 336 |
| Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu |     |
| 100 105 110   |     |
| CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG GTG ACG GGA | 384 |
| His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val Thr Gly |     |
| 115 120 125   |     |
| GAG GAA GAC TCT GCC CTG GGA AGA ACG GGC CCC ACC CTG GCC ATG AAG | 432 |
| Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Met Lys |     |
| 130 135 140   |     |
| AGG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAT AGT | 480 |
| Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser |     |
| 145 150 155 160   |     |



GAC TGC GCC TGG GAA ATT GTC AGA CTG GAA ATC ATG AGA TCC TTG TCT 528  
 Asp Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg Ser Leu Ser  
 165 170 175

TCA TCA ACC AGC TTG CAC AAA AGG TTA AGA ATG ATG GAT GGA GAC CTG 576  
 Ser Ser Thr Ser Leu His Lys Arg Leu Arg Met Met Asp Gly Asp Leu  
 180 185 190

AGC TCA CCT TGA 588  
 Ser Ser Pro  
 195

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
 of SEQ ID NO:31 (HuIFNtau3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
 1 5 10 15

Gly Pro Gly Gly Ser Leu Arg Cys Asp Leu Ser Gln Asn His Val Leu  
 20 25 30

Val Gly Ser Gln Asn Leu Arg Leu Leu Gly Gln Met Arg Arg Leu Ser  
 35 40 45

Leu Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Phe Pro Gln Glu  
 50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
 65 70 75 80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu  
100 105 110

His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val Thr Gly  
115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Met Lys  
130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg Ser Leu Ser  
165 170 175

Ser Ser Thr Ser Leu His Lys Arg Leu Arg Met Met Asp Gly Asp Leu  
180 185 190

Ser Ser Pro  
195

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence

000001 010517260

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|   |     |
|---|-----|
| TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG | 48  |
| Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg |     |
| 1 5 10 15   |     |
| CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC | 96  |
| Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp |     |
| 20 25 30  |     |
| AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC | 144 |
| Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu |     |
| 35 40 45  |     |
| CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC | 192 |
| Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser |     |
| 50 55 60  |     |
| TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC | 240 |
| Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr |     |
| 65 70 75 80   |     |
| CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG | 288 |
| Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu |     |
| 85 90 95  |     |
| GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA | 336 |
| Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly |     |
| 100 105 110   |     |
| AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT | 384 |
| Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His |     |
| 115 120 125   |     |
| GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC | 432 |
| Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val |     |
| 130 135 140   |     |

AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA 480  
 Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys  
 145 150 155 160

AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT TG 518  
 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro  
 165 170

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg  
 1 5 10 15  
 Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp  
 20 25 30  
 Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu  
 35 40 45  
 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser  
 50 55 60  
 Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr  
 65 70 75 80  
 Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu  
 85 90 95  
 Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly  
 100 105 110

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
34-64 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu Gln  
1 5 10 15

Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser  
20 25 30

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
62-92 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp  
1 5 10 15

Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln  
20 25 30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
90-122 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val Thr Gly  
1 5 10 15

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Met Lys  
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
119-150 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Met Lys Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys  
1 5 10 15

Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg  
20 25 30

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
139-172 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg Ser Leu Ser Ser  
1                      5                      10                      15

Ser Thr Ser Leu His Lys Arg Leu Arg Met Met Asp Gly Asp Leu Ser  
20                      25                      30

Ser Pro

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
1-23 of SEQ ID NO:32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:



Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
1 5 10 15

Gly Pro Gly Gly Ser Leu Arg  
20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
1-23 of SEQ ID NO:11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
1 5 10 15

Gly Pro Gly Gly Ser Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau1 genomic-derived  
DNA coding sequence, without leader seq.

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|   |     |
|---|-----|
| TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGG AAG AAC CTC AGG | 48  |
| Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg |     |
| 1 5 10 15   |     |
| CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG CAG GAC | 96  |
| Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp |     |
| 20 25 30  |     |
| AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC | 144 |
| Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu |     |
| 35 40 45  |     |
| CAG GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC | 192 |
| Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser |     |
| 50 55 60  |     |
| TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC | 240 |
| Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr |     |
| 65 70 75 80   |     |
| CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAC AAC CTG | 288 |
| Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu |     |
| 85 90 95  |     |
| GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG GAA GAC TCT GCC CTG GGA | 336 |
| Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly |     |
| 100 105 110   |     |
| AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG GGC ATC CAT | 384 |
| Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His |     |
| 115 120 125   |     |

GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC 432  
 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val  
 130 135 140

AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA 480  
 Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu  
 145 150 155 160

AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA 519  
 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro  
 165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg  
 1 5 10 15

Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp  
 20 25 30

Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu  
 35 40 45

Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser  
 50 55 60

Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr  
 65 70 75 80

Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu  
 85 90 95

